

Figure 1

|    | <u>Gene symbol</u> | <u>Gene name</u>   |
|----|--------------------|--|
| 5  | OSBP               | Oxysterol-binding protein  |
|    | NFKB3<br>(p65)     | nuclearfactor of kappa light polypeptide gene enhancer B-cells 3 |
| 10 | CAPN1              | Calpain, large polypeptide L1                                    |
|    | CCND1              | Cyclin D1  |
| 15 | EFEMP2*            | EGF-containing fibulin-like extracellular matrix protein 2       |
|    | FOSL1              | FOS-like antigen-1   |
|    | PLCB3              | Phospholipase C, beta 3 (phosphatidylinositol-specific)          |
| 20 | PPP1CA             | Protein phosphatase-1, catalytic subunit, alpha isoform          |
|    | VEGFB              | Vascular endothelial growth factor B                             |
| 25 | ESRRA, ERR1        | estrogen-related receptor alpha                                  |
|    | CTSW               | Cathepsin W  |
|    | GALN*              | Galanin  |
| 30 | LRP5, LRP7, LR3*   | Low density lipoprotein receptor-related protein-5               |
|    | CBP2               | Collagen-binding protein 2 (colligen 2)                          |
| 35 | TCIRG1             | T-cell immune regulator 1  |
|    | LTBP3              | Latent transforming growth factor-beta binding protein-3         |
|    | FGF19*             | Fibroblast growth factor 19 (FGF19)                              |
| 40 | Delta5-desaturase* | Delta5-desaturase  |

Figure 2

GCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCGGACAACAT  
GGAGGCAGCGCCCGCCCGGGCCCGCGTGGCCGCTGCTGCTGCTGCTGCTGCT  
5 GCTGGCGCTGTGCGGCTGCCCGGCCCCCGCGCGGCGCTCGCCGCTCCTGCTATT  
GCCAACC CGCGGGACGTACGGCTGGTGGACCGCGCGGAGTCAAGCTGGAGTC  
CACCATCGTGGTCAGCGGCTGGAGGATGCGGCCGAGTGGACTTCCAGTTTTC  
CAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCT  
ACCTGAACCAGACGGGGCGCGCGTGCAGAACGTGGTCACTCCCGGCTGGTCT  
10 CTCCGACGGCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACT  
CAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGC  
TCTTCTGGCAGGACCTTGACCAGCCTAGGGCCATCGCCTTGGACCCCGCTCAG  
GGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGATTGAGCGGGCAGGG  
ATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAAT  
15 GGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTC  
AGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAG  
GGCAGCCTGACGCACCCCTTCGCCCTGACGGCTCTCCGGGGACACTCTGTACTGG  
ACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAG  
AGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGC  
20 CAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGC  
TCCCACCTGTGCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCTGCCCA  
CGGGTGTGAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAG  
GTGCTGCTGCTGGCCCCGGCGGACGGACCTAGCGGAGGATCTCGCTGGACACGCCG  
GACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCAATTGCCATC  
25 GACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCC  
ATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACCGCTGGTCAACACCGAG  
ATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGG  
ACCGACAGGGGACCGGACCGCATCGAGGTGACCGCGCTCAACGGCACCTCCCCG  
AAGATCCTGGTGTGGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCC  
30 GTGATGGGCTCATGTACTGGACAGACTGGGGAGAGAAACCTAAATCGAGTGT  
GCCAACTTGGATGGGCAGGAGCGGGTGTGCTGGTCAATGCCTCCCTCGGGTGG  
CCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCC  
AAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGCGGACCCCT  
CCTGGAGGACAAGCTCCCCGCACATTTTCGGGTTACCGCTGCTGGGGGACTTCAT  
35 CTACTGGACTGACTGGCAGCGCCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGC  
CAGCCGGGACGTCAATGACCAGCTGCCCGACCTGATGGGGCTCAAGCTGT  
GAATGTGGCCAAGGTGCTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGT  
GCAGCCACCTGTGCTTCTTACACCCACGCAACCCCGGTGTGGCTGCCCATCG  
GCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGG  
40 TCTTACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACG  
ACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGGCTCAGCCCTGGACTTTGATG  
TGTCCAACAACCACATCTACTGGACAGACGTCAAGCCTGAAGACCATCAGCCGG  
CCTTCATGAACGGGAGCTCGGTGGAGCAGTGGTGGAGTTTGGCCTTGACTACC  
CCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTG  
45 GGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAAGTTCCGGCAAGTCCTC  
GTGTGGAGGGACTTGGACAACCCGAGGTGCTGCCCCTGGATCCACCAAGGGC  
TACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATG

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GACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCGGGCCCAACGACCT  
CACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACAT  
GATCGAGTCGTCCAACATGCTGGGTGAGGAGCGGGTCGTGATTGCCGACGATCT  
CCCCACCCGTTCCGGTCTGACGCGAGTACAGCGATTATATCTACTGGACAGACTG  
5 GAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGGCCGGAACCGCACCCCT  
CATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCTCTCCCGC  
CAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGC  
CTTGCCATCCCCGGCGGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGAC  
CCCAGCAGCCGCAACTGCAGCCCCGCCACCACCTTCTTGCTGTTACGCCAGAAA  
10 TCTGCCATCAGTCGGATGATCCCGGACGACCAGCACAGCCCCGGATCTCATCCTG  
CCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAG  
TTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGG  
GACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCA  
GCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGA  
15 GGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGG  
TGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGA  
GGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCA  
GCCCTGGACGGCACCGAGCGCGAGGTCTCTTACCACCGGCCTCATCCGCCCT  
GTGGCCCTGGTGGTGGACAACAACACTGGGCAAGCTGTTCTGGGTGGACGCGGAC  
20 CTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAG  
GACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTAC  
TGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGA  
CAAGCGGACTCGCATCCAGGGCCGTGTCGCCACCTCACTGGCATCCATGCAGT  
GGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCCACCCATGTGCCCGTGACAATGG  
25 TGGCTGCTCCACATCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATG  
CCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCAC  
CTGCTCCCCGGACCAAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGG  
GGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGG  
CTGCCCCGTGTGCTCCGCCGCCAGTTCCCCTGCGCGCGGGGTGAGTGTGTGGA  
30 CCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGC  
GGACTGTGACGCCATCTGCCTGCCCAACCAAGTTCCGGTGTGCGAGCGGGCAGTG  
TGTCCTCATCAAACAGCAGTGGGACTCCTTCCCCGACTGTATCGACGGCTCCGA  
CGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCCGGCCCCACAG  
CAGTGCCATCGGGCCCCGTCAATTGGCATCATCCTCTCTCTCTTCGTATGGGTGGT  
35 GTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGGCCAACGGG  
CCCTTCCCCGCACGAGTATGTGACGGGACCCCGCACGTGCCCTCAATTTTATA  
GCCCCGGGCGGTTCCCAGCATGGCCCCTTACAGGCATCGCATGCGGAAAGTCC  
ATGATGAGCTCCGTGAGCCTGATGGGGGGCGGGGCGGGGTGCCCTGTACGAC  
CGGAACCACGTACAGGGGCCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACG  
40 CTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTG  
TACAACATGGACATGTTCTACTCTTCAAACATTCGGGCCACTGCGAGACCGTAC  
AGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGAC  
GTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTG  
GATTTGAACTCGGACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAG  
45 TACCTGTGCGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTAC  
TTCCATCTCTTCCCGCCCCCTCCGTCCCC  
CTGCACGGACTCATCCTGACCTCGGCCGGGGCCACTCTGGCTTCTCTGTGCCCTG  
TAAATAGTTTTAAATATGAACAAAGAAAAAATATATTTTATGATTTAAAAAAT

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AAATATAATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGC  
AGGGCTGGGAGAACTTTGTA

Figure 3

MEAAPPGPPWPLLLLLLLLLLALCGCPAPAAASPLLLFANRRDVRLVDAGGVKLESTI  
VVSGLEDAAAVDFQFSKGAVYWTDVSEEAJKQTYLNQTGAAVQNVVISGLVSPDGL  
5 ACDWVGKKLYWTDSETNRIEVANLNGTSRKVLFWQDLDQPRAIALDPAHGYMYW  
TDWGETPRIERAGMDGSTRKIIVDSDIYWPNGLTIDLEEKLYWADAKLSFIHRANL  
DGSFRQKVVEGSLTHPFALTLSGDTLYWTDWQTRSIHACNKRTGGKRKEILSALYSP  
MDIQVLSQERQPFHTRCEEDNGGCSHLCLLSPSEPFYTCACPTGVQLQDNGRTCKA  
GAEEVLLLARRTDLRRISLDTPDFTDIVLQVDDIRHAIAIDYDPLEGYVYWTDDEVR  
10 AIRRAYLDGSGAQT LVNTEINDPDGIAVDWVARNLYWTDGTGTDRIEVTRLNGTSRK  
ILVSEDLDPEPRAIALHPVMGLMYWTDWGENPKIECANLDGQERRVLVNASLGWPN  
GLALDLQEGKLYWGDADKTDKIEVINVDGTKRRTLLEDKLPHIFGFTLLGDFIYWTD  
WQRRSIERVHKVKASRDVIIDQLPDLMLGKAVNVAKVVGTPNCAADRNGGCSHLCHF  
TPHATRCGCPIGLELLSDMKTCIVPEAFLVFTSRAAJHRISLETNNNDVAIPTGVKE  
15 ASALDFDVSNNHIYWTDVSLKTISRAFMNGSSVEHVVEFGLDYPEGMAVDWMGKN  
LYWADTGTNRIEVARLDGQFRQVLVWRDLNPRSLALDPTKGYTYWTEWGGKPRI  
VRAFMDGTNCMTLVDKVGRANDLTIDYADQRLYWTDLDTNMIESSNMLGQERVV  
IADDLPHPFGLTQYSDIYWTDWNLHSIERADKTSGRNRTLIQGHLD FVMDILVFHS  
SRQDGLNDCMHNNGQCGQLCLAIPGGHRCGCASHYTLDPSSRNCSPPTTFLFSQKS  
20 AISRMIPDDQHSPDLILPLHGLRNVKAIDYDPLDKFIYWVDGRQNIKRAKDDGTQPF  
VLTSLSQGQNPDRQPHDLSIDIYSRTLFWTCEATNTINVHRLSGEAMGVVLRGDRDK  
PRAIVVNAERGYLYFTNMQDRAAKJERAALDGTREVLFTTGLIRPVALVVDNTLG  
KLFWVDADLKRIESCDLSGANRLTLEDANIVQPLGLTILGKHLWIDRQQQMIEVE  
KTTGDKRTRIQRVAHLTGHAHAVEEVSLEEFSAHPCARDNNGGCSHICIAKGDGTPRC  
25 SCPVHLVLLQNLLTCGEPPTCSPDQFACATGEIDCIPGAWRCDFPECDQSDDEEC  
PVCSAAQFPCARGQCVDLRLRCDGEADCQDRSDEADCAICLPNQFRCASGQCCLI  
KQQCDSFPDCIDGSDELMCEITKPPSDDSPAHS SAIGPVIGIILSLFVMGGVYFVCQRV  
VCQRYAGANGPFPHEYVSGTPHVPLNFIA PGGSQHGPFTGIACGKSMMSSVSLMGG  
RGGVPLYDRNHVTGASSSSSSTKATLYPPILNPPPSPATDPSLYNMDMFYSSNIPAT  
30 ARPYRPNIRGMAPPPTTPCSTDVCDSDYSASRWKASKYYLDLNSDSDPYPPPTPHSQ  
YLSAEDSCPPSPATERSYFHLFPPPPSPCTDSS

Figure 4

| Source  | Nucleotide change                 | Protein change                    | Putative effect          |
|---------|-----------------------------------|-----------------------------------|--------------------------|
| OPS 88  | G29A                              | Trp10stop                         | Truncation               |
| Control | A459G                             | Pro153Pro                         | No change                |
| Control | InsCTG33                          | Insert Leu<br>at residue 12       | Alters signal<br>peptide |
| OPS 78  | GACCTACG<br>1051-1058<br>ACCCTACA | AspLeuSer<br>351-353<br>ThrLeuLys | Unknown                  |
| OPS 59  | C1282T                            | Arg428stop                        | Truncation               |
| OPS 53  | G1253T                            | Glu485stop                        | Truncation               |
| OPS 23  | delG1467                          | Frameshift                        | Truncation               |
| OPS 82  | G1481A                            | Arg494Gln                         | Unknown                  |
| OPS 2   | C1708T                            | Arg570Trp                         | Unknown                  |
| OPS 72  | G1999A                            | Val677Met                         | Unknown                  |
| OPS 45  | insT2150                          | Frameshift                        | Truncation               |
| OPS 41  | G2202A                            | Trp734stop                        | Unknown                  |
| Control | C2220T                            | Asn740Asn                         | Unknown                  |
| OPS 92  | delG2305                          | Frameshift                        | Truncation               |
| OPS13   | C2557T                            | Gln853stop                        | Truncation               |
| OPS 7   | delA3804                          | Frameshift                        | Truncation               |
| OPS 53  | C3989T                            | Ala1330Leu                        | Unknown                  |
| OPS 72  | C3989T                            | Ala1330Leu                        | Unknown                  |
| Control | G4416T                            | Leu1472Leu                        | No change                |

Figure 5

| NAME      | SEQUENCE                          | LOCATION | PRODUCT<br>SIZE |
|-----------|-----------------------------------|----------|-----------------|
| LRGEN1F   | 5'-TTG CTG CCC TAG ACT TAG CC-3'  | -119     | 406             |
| LRGEN1R   | 5'-CCA AGT CGC TTC CGA GAC-3'     | +106     |                 |
| LRGEN2F   | 5'-CAT CCC AGG GCT GTG TAT CT-3'  | -65      | 543             |
| LRGEN2R   | 5'-ACT TGG GCT CAT GCA AAT TC-3'  | +81      |                 |
| LRGEN3F1  | 5'-CCG ATG GGT GAG ATT TTA GG-3'  | -118     | 329             |
| LRGEN3R1  | 5'-CGT GGG TAC CTA CCG GAA C-3'   | +16      |                 |
| LRGEN4NF  | 5'-TAA TTG GGT CAG CAG CAA TG-3'  | -72      | 277             |
| LRGEN4NR  | 5'-GCA CTC ACA GAA AGG CTG-3'     | +8       |                 |
| LRGEN5NF  | 5'-AGT GAC GGT CCT CTT CTG GA-3'  | -51      | 302             |
| LRGEN5NR  | 5'-CAA GTG GAT CAT TTC GAA CG-3'  | +120     |                 |
| LRGEN6F   | 5'-TGG CTG AGT ATT TCC CTT GC-3'  | -95      | 577             |
| LRGEN6R   | 5'-CCA GAA TGA CAG GTC CAG GT-3'  | +85      |                 |
| LRGEN7F1  | 5'-TGC TTC TTC TCC AGC CTC AT-3'  | -14      | 302             |
| LRGEN7R1  | 5'-ATG TGG CCA AAT AGC AGA GC-3'  | +116     |                 |
| LRGEN8F   | 5'-GCA TTG AAC CCG TCT TGT TT-3'  | -109     | 426             |
| LRGEN8R   | 5'-GGC ACC TGA GCT CAA CAC TT-3'  | +100     |                 |
| LRGEN9F   | 5'-TGC TGG GCT GTT GT GTT TA-3'   | -47      | 407             |
| LRGEN9R   | 5'-CTT TGA GGC AGG AAC AGA GG-3'  | +70      |                 |
| LRGEN10F  | 5'-AGC GAA ACT CCG TCT CAA AA-3'  | -79      | 417             |
| LRGEN10R  | 5'-GCT CTA ATC ACT GAG GGC CA-3'  | +110     |                 |
| LRGEN11F1 | 5'-GAG GGC TGA GCT GAA GAG GT-3'  | -105     | 398             |
| LRGEN11R1 | 5'-CAG GTT GGG GAA CTT GCA G-3'   | +108     |                 |
| LRGEN12F  | 5'-ATT CAT GTG GTC GCT AGG CT-3'  | -113     | 479             |
| LRGEN12R  | 5'-GAA GCT CCT TTC AGC GTC AG-3'  | +40      |                 |
| LRGEN13F  | 5'-CCA GCT CCT CTG TGG CTT AC-3'  | -57      | 352             |
| LRGEN13R  | 5'-TCC TCC CTC TGC TAA GGA CA-3'  | +95      |                 |
| LRGEN14F  | 5'-CAG AGC TCT CCA GCC AGT G-3'   | -149     | 440             |
| LRGEN14R  | 5'-CTG TGA GAG GCT GGC ATT C-3'   | +82      |                 |
| LRGEN15NF | 5'-ATG TGA CCT GTC AGC CTC G-3'   | -131     | 415             |
| LRGEN15NR | 5'-TGC TGC CAT TAC TGA CAA TGA-3' | +83      |                 |
| LRGEN16F  | 5'-TCT GTC CTC CCA AGC TGA GT-3'  | -76      | 374             |
| LRGEN16R  | 5'-CAC ACA GGA TCT TGC ACT GG-3'  | +88      |                 |
| LRGEN17F  | 5'-CAT GAG TTC TCA TTT GGC CC-3'  | -92      | 321             |
| LRGEN17R  | 5'-GCC ACA GGG ACT GTG ATT TT-3'  | +103     |                 |
| LRGEN18F  | 5'-CAA CTT CTG CTT TGA AGC CC-3'  | -88      | 423             |
| LRGEN18R  | 5'-CAG AGC CCC TAC TCC TGT GA-3'  | +98      |                 |
| LRGEN19F  | 5'-CCA GAC CTT GGT TGC TGT G-3'   | -81      | 269             |
| LRGEN19R  | 5'-CGT CTC CTC CCC TAA ACT CC-3'  | +77      |                 |
| LRGEN20NF | 5'-ATG TTG GCC ACC TCT TTC TG-3'  | -34      | 310             |
| LRGEN20NR | 5'-CTG CCT CCT CCA GAT CAT TC-3'  | +39      |                 |
| LRGEN21F  | 5'-GAG TCT CGT GGG TAG TGG GA-3'  | -102     | 373             |

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|          |                                   |      |     |
|----------|-----------------------------------|------|-----|
| LRGEN21R | 5'-AGA AAG CAA GCA TGC CTC AG-3'  | +131 |     |
| LRGEN22F | 5'-AGC CCT CTC TGC AAG GAA AG-3'  | -96  | 305 |
| LRGEN22R | 5'-GCC CAC TAG CAC CCA GAA TA-3'  | +111 |     |
| LRGEN23F | 5'-GAC AGG CCT TTC CCG TTC-3'     | -95  | 650 |
| LRGEN23R | 5'-CAG GAG GAC TCT CAT GGT GG-3'  | +106 |     |
| LRCOD1F  | 5'-TTC GTC ATG GGT GGT GTC TA-3'  | 4192 | 416 |
| LRCOD1R  | 5'-TTC CTC GAA TGA TGT AGG GC-3'  | 4607 |     |
| LRCOD2F  | 5'-ACC TGG ACT TCG TGA TGG AC-3'  | 2654 | 466 |
| LRCOD2R  | 5'-CAG AAC AGT GTC CGG CTG TA-3'  | 3119 |     |
| LRCOD3F  | 5'-CCA TGG AGC CCG AGT GAG-3'     | -50  | 504 |
| LRCOD3R  | 5'-GTC AAG GTC CTG CCA GAA GA-3'  | 453  |     |
| LRCOD4F  | 5'-GGG CAA GAA GCT GTA CTG GA-3'  | 354  | 500 |
| LRCOD4R  | 5'-TGG ATG TCC ATG GGT GAG TA-3'  | 853  |     |
| LRCOD5F  | 5'-CAG ACC CGC TCC ATC CAT-3'     | 767  | 484 |
| LRCOD5R  | 5'-TCG TTG ATC TCG GTG TTG AC-3'  | 1250 |     |
| LRCOD6F  | 5'-ATC GAC TAC GAC CCG CTA GA-3'  | 1132 | 546 |
| LRCOD6R  | 5'-GTA GAT GAA GTC CCC CAG CA-3'  | 1677 |     |
| LRCOD7F  | 5'-GCC AAG ACA GAC AAG ATC GAG-3' | 1564 | 505 |
| LRCOD7R  | 5'-TGT GGT TGT TGG ACA CAT CA-3'  | 2068 |     |
| LRCOD8F  | 5'-CAC AGG ATC TCC CTC GAG AC-3'  | 1966 | 522 |
| LRCOD8R  | 5'-CTC GAT CAT GTT GGT GTC CA-3'  | 2487 |     |
| LRCOD9F  | 5'-CAG CCC TTT GTT TTG ACC TC-3'  | 3025 | 484 |
| LRCOD9R  | 5'-TCC AGT AGA GAT GCT TGC CA-3'  | 3508 |     |
| LRCOD10F | 5'-AAG CGC ATT GAG AGC TGT G-3'   | 3400 | 480 |
| LRCOD10R | 5'-CTC CTC GTC GCT CTG GTC-3'     | 3879 |     |
| LRCOD11F | 5'-CAC AGG GGA GAT CGA CTG TAT-3' | 3801 | 480 |
| LRCOD11R | 5'-ACA TAC TCG TGC GGG AAG G-3'   | 4280 |     |
| LRCOD12F | 5'-GTC CAG CAG CTC GTC CAG-3'     | 4446 | 567 |
| LRCOD12R | 5'-TAC AAA GTT CTC CCA GCC CT-3'  | 5012 |     |
| LRCOD13F | 5'-TCA TGG ACG GGA CCA ACT-3'     | 2369 | 431 |
| LRCOD13R | 5'-GGT GTA GTG TGA GGC GCA G-3'   | 2799 |     |



## Figure 6

### BMSR Construct Information

5 The following BSMR expression constructs have been constructed using the pcDNA3 expression vector for use in following BSMR expression, function, and other biological (e.g. ligand and downstream signaling) interactions.

10 1. A full length wild type construct extending from primers LRCOD3F to LRCOD12R.

15 Sequence encoding a FLAG antibody epitope (GAC TAC AAG GAC GAC GAT GAC AAG) was inserted into the wild-type construct immediately downstream of nucleotide 165 (relative to the "A" in the ATG translation start site). This construct expresses a BSMR protein which has a FLAG epitope between wild type BSMR amino acid residues 55 and 56.

This was accomplished using the following primer sequences and a Quickchange reaction:

20 LRPFLAGF: 5'-GAC TAC AAG GAC GAC GAT GAC AAG ACC ATC GTG GTC AGC GGC CTG-3'

25 LRPFLAGR: 5'-CTT GTC ATC GTC GTC CTT GTA GGA CTC CAG CTT GAC TCC GCC-3'

Sequence encoding a MYC antibody epitope (GAG CAG AAG CTG ATA TCC GAG GAG GAC CTG) was inserted immediately upstream of the stop codon after residue 4845 (relative to the "A" in the ATG translation start site). The construct expresses a BSMR protein which has a MYC epitope at the end of the wild type BSMR polypeptide.

30 This was accomplished using the following primer sequences and a Quickchange reaction:

35 LRPMYCF: 5'-GAG CAG AAG CTG ATA TCC GAG GAG GAC CTG TGA CCT CGG CCG GGC-3'

LRPMYCR: 5'-CAG GTC CTC CTC GGA TAT CAG CTT CTG CTC GGA TGA GTC CGT GCA-3'

40 A expression construct containing both the FLAG and MYC antibody epitopes at the aforementioned sites has also been produced.

Figure 7

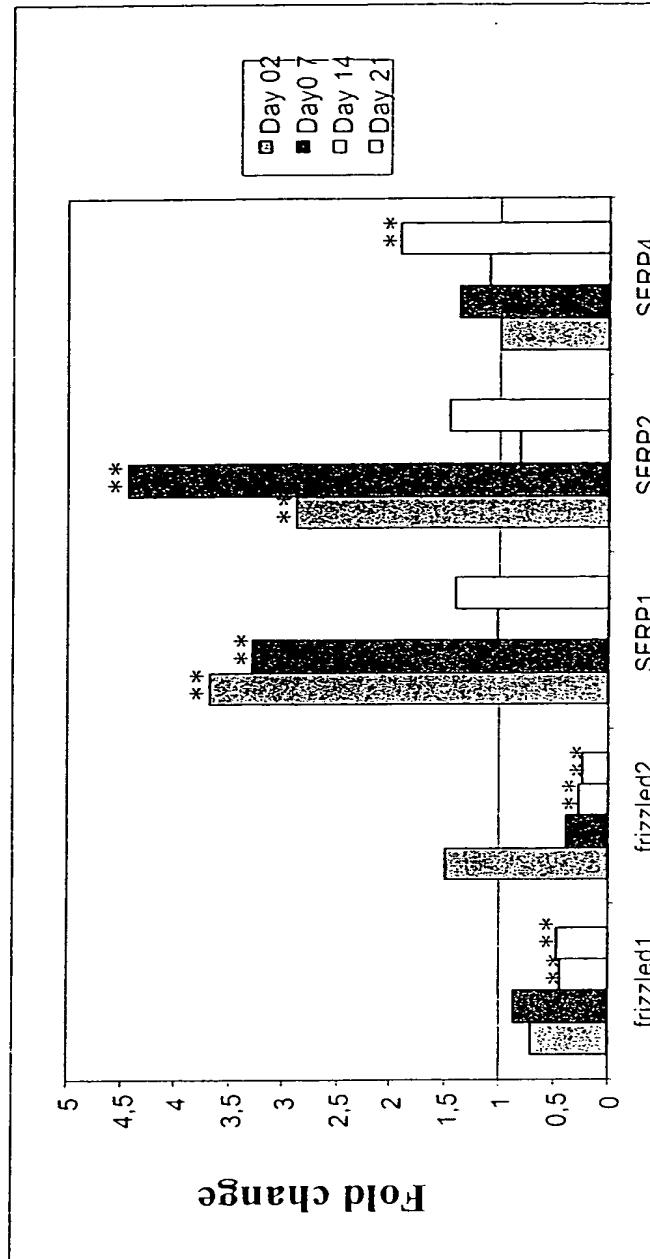


Figure 8

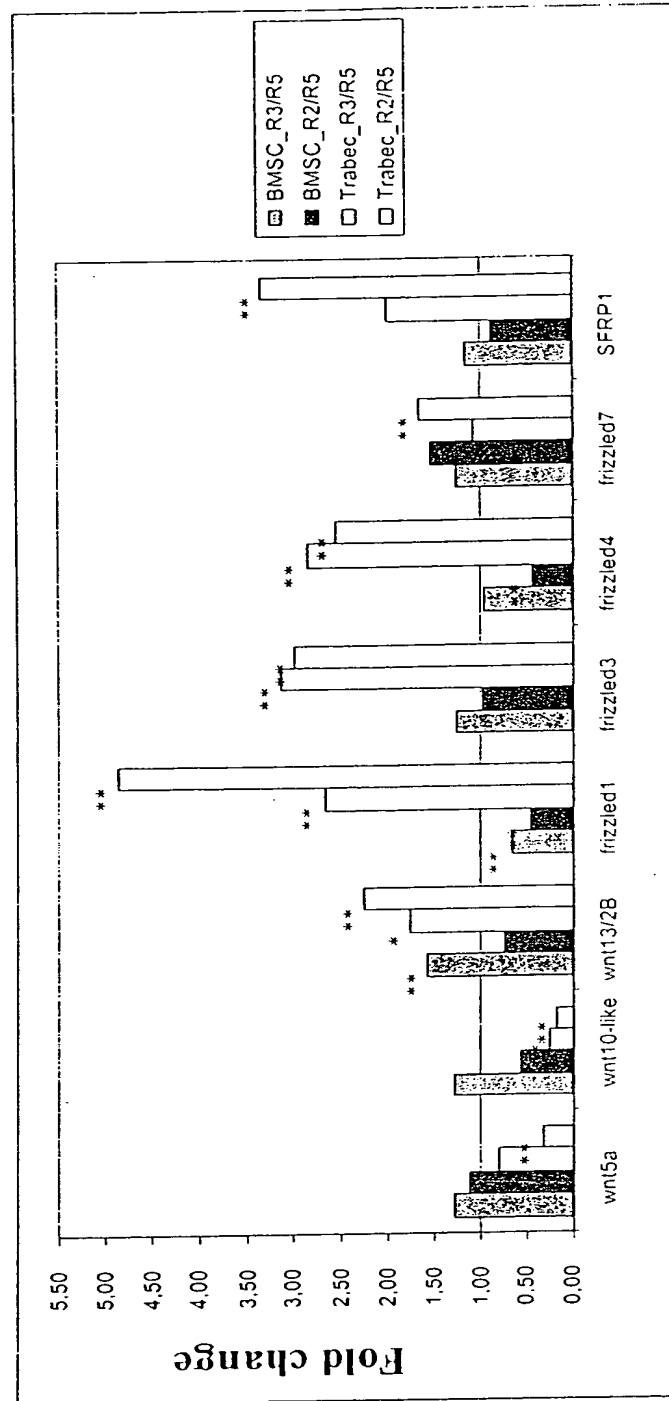


Figure 9

| Cell line/treatment<br>Gene name | C2C12/BMP2<br>(4 days) | C3H10T1/2/BMP2+SHH<br>(4 days) | ST2/BMP2<br>(4 days) | MC3T3-E1<br>(3 days)         |
|----------------------------------|------------------------|--------------------------------|----------------------|------------------------------|
| Frizzled-1                       | 2.25 x                 | NR                             | 2.62x                | 2.11x                        |
| Frizzled-4                       | NR                     | 437x                           | NR                   | NR                           |
| SFRP2/SARP1                      | 8.10 x                 | 0.5x<br>(0.4x with SHH alone)  | 8.54x                | 3.61x<br>(0.09 with TGFbeta) |

Figure 10

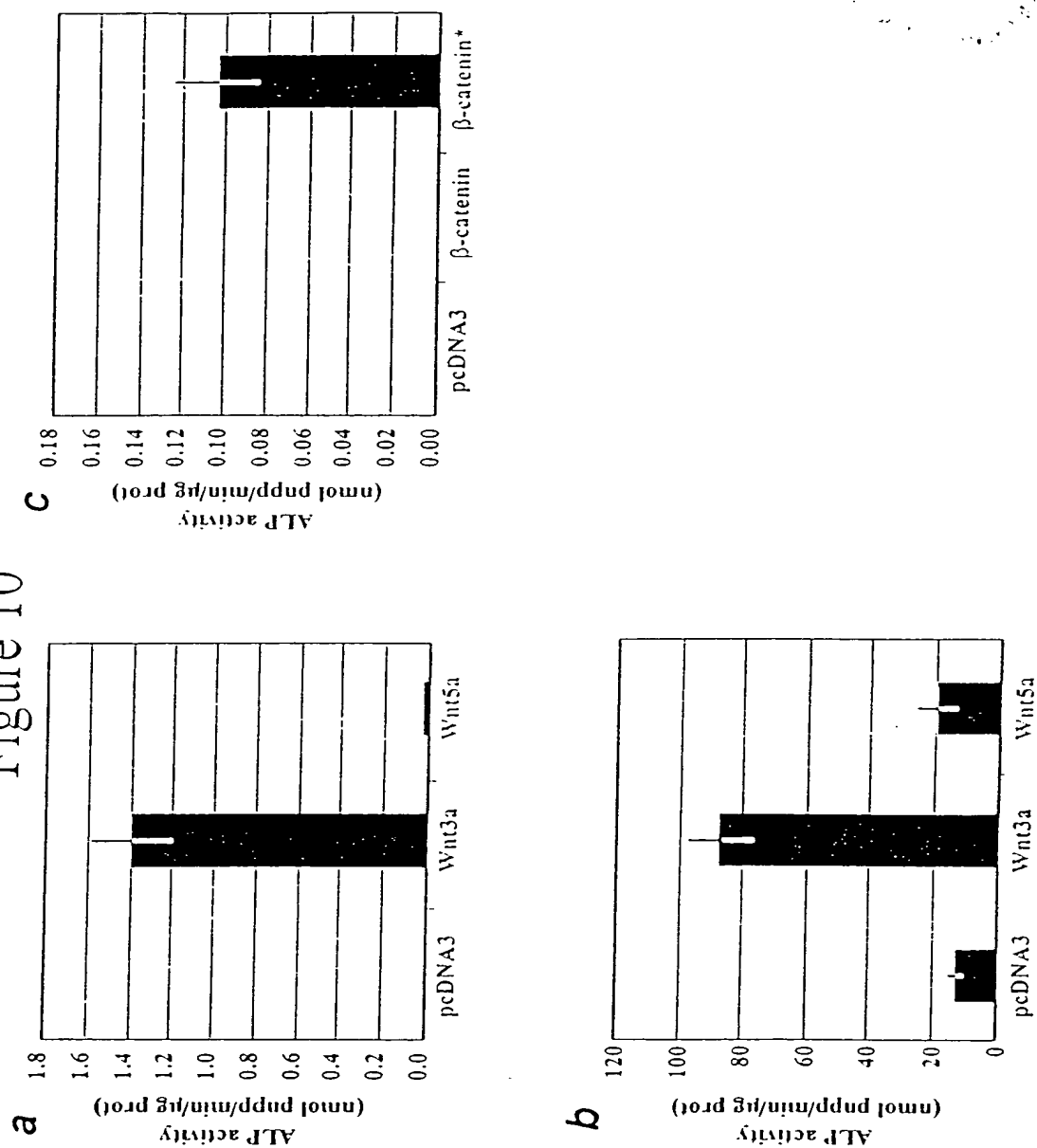
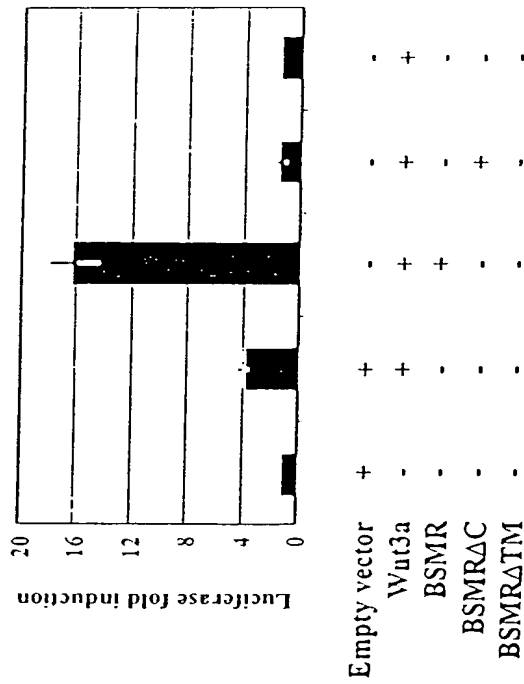
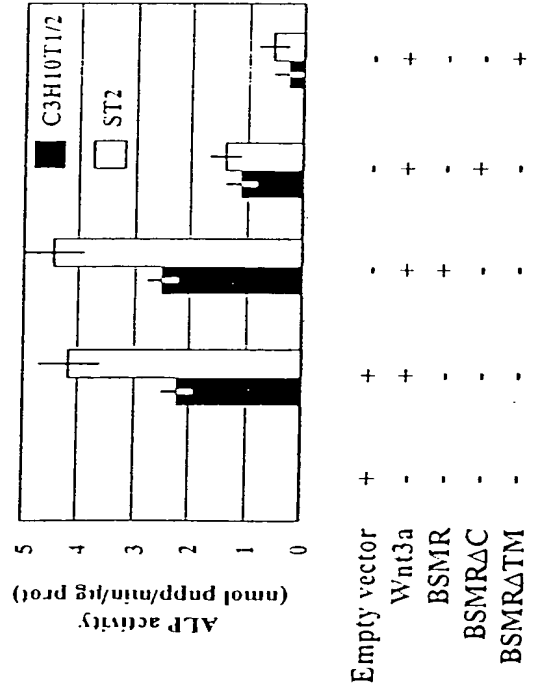


Figure 11

a



b



c

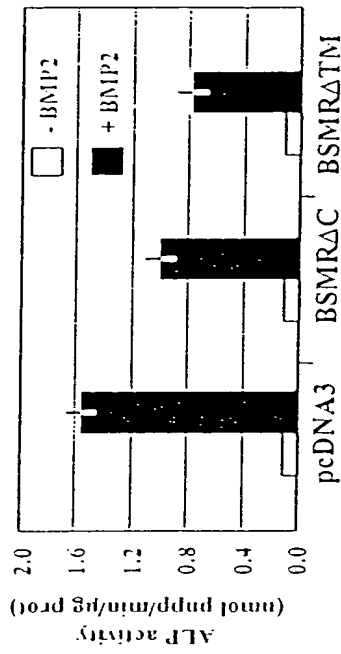
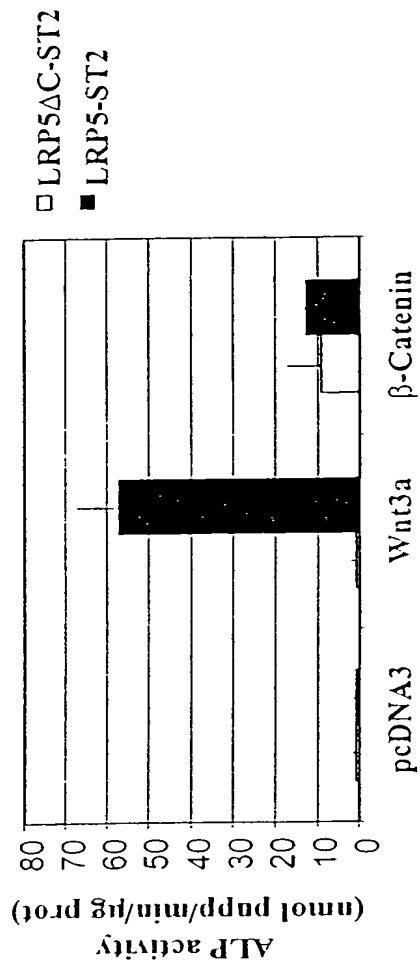


Figure 12



## Figure 13

RVRLASHLRKLRK

RLTRKRGLKLA

CRAKRNNFKSA

LKWKS

KIRVKAGETQKKVIFCSREKVSHL

FIPLKPTVKMLERSNHVSRTEVSSNHV

DKGMAPALRHLYKELMGPWN

DALKLAIDNALSIT